galactosidase from the reporter gene and identifying that promoter set showing the weakest β-galactosidase activity, to the strongest activity that is detectable by the same procedure with the exception that the promoter of the promoter set showing the strongest activity in said reporter gene system is identified, each promoter sequence of said set of promoter sequences comprising a double stranded DNA sequence, the sense strands of which comprise

at least two consensus sequences, said at least two consensus sequences corresponding to conserved sequences identified in said organism or group of organisms, at least half of each of said consensus sequences being kept constant in the set of promoter sequences, the at least two consensus sequences, when the selected organism or group of organisms is prokaryotic, being selected from the group consisting of TATAAT, TATRAT, TTGACA and an activator binding site upstream of the TATAAT sequence (a UAS) and the at least two consensus sequences, when the selected organism or group of organisms is eukaryotic, being selected from the group consisting of a TATA-box and a UAS upstream of said TATA-box and, between said consensus sequences or flanking at least one of said consensus sequences, at least one nucleotide spacer sequence, at least part of which, relative to the corresponding spacer sequence of the identified promoter, is varied by random incorporation of nucleotides that are selected from the group consisting of the nucleobases A, T, C and G,

the set of promoter sequences covering the range of promoter activities for said gene, in steps, each step changing the activity by 50-100%.

16. (Twice Amended) A method of constructing a set of promoter sequences which is suitable for optimizing the expression of a gene in a selected organism or group of organisms, the method comprising the steps of

(i) identifying in said organism or group of organisms a promoter sequence comprising at least two consensus sequences, which consensus sequences correspond to conserved sequences identified in said organism or group of organisms, at least one of the consensus sequences being flanked by a non-conserved nucleotide spacer sequence or

both or said consensus sequences being separated by the non-conserved nucleotide spacer sequence,

(ii) constructing a set of single stranded DNA sequences comprising at least half of each of the consensus sequences, and a non-conserved nucleotide spacer sequence, at least part of which is varied by a random incorporation of nucleotides selected from the group consisting of the nucleobases A, T, C and G, whilst keeping the at least half of the consensus sequences constant, and

(iii) converting the single stranded DNA sequences into double stranded DNA sequences to obtain the set of promoter sequences covering, with respect to promoter strength, a range of promoter activities which is within a range from the weakest activity that is detectable by inserting each of the set of promoters into a vector comprising a promoterless β-galactosidase reporter gene system, transforming a host strain with the resulting vector and cultivating the transformed host strain with the resulting vector and cultivating the transformed host strain to express β-galactosidase from the reporter gene and identifying that promoter set showing the weakest β-galactosidase activity, to the strongest activity that is detectable by the same procedure with the exception that the promoter of the promoter set showing the strongest activity in said reporter gene system is identified.

18. (Thrice Amended) A method of controlling in an organism the flux of a cellular metabolite or the expression of a desired gene product, said method comprising at least one step of changing the expression level of at least one gene in the pathway leading to formation of said metabolite or the expression level of said desired gene product, the step comprising

(i) selecting from the set of promoter sequences of claim 1 a plurality of promoter sequences covering a desired range of promoter activities,

(ii) transforming said set of promoter sequences into cells of the organism, placing in each of said cells the gene to be expressed under the control of at least one promoter of the set,

(iii) cultivating the transformed cells to obtain clones thereof and selecting among said clones a clone having, relative to an otherwise identical clone where the at least one gene in the pathway or the gene expressing the desired gene product is under the control of its native promoter, a higher or a lower flux of the cellular metabolite or a higher or a lower expression of the desired gene product.

21. (Thrice Amended) A method of isolating a promoter sequence being capable of optimizing the expression of a gene in a selected organism, the method comprising

(i) constructing, using the method of claim 16, a set of promoters covering, with respect to promoter strength, a range of promoter activities which is within a range from the weakest activity that is detectable by inserting each of the set of promoters into a vector comprising a promoterless β-galactosidase reporter gene system, transforming a host strain with the resulting vector and cultivating the transformed host strain with the resulting vector and cultivating the transformed host strain to express β-galactosidase from the reporter gene and identifying that promoter set showing the weakest β-galactosidase activity, to the strongest activity that is detectable by the same procedure with the exception that the promoter of the promoter set showing the strongest activity in said reporter gene system is identified,

(ii) transforming said set of promoters into cells of the selected organism, placing in each of said cells the gene to be expressed under the control of at least one promoter of the set,

(iii) cultivating the transformed cells to obtain clones thereof and selecting among said clones a clone having, relative to an otherwise identical clone where the at least one gene in the pathway or the gene expressing the desired gene product is under the control of its native promoter, a higher or a lower flux of the cellular metabolite or a higher or a lower expression of the desired gene product, and

(iv) isolating said promoter sequence from the clone.

Please add the following claims:

23. (New) A set of promoters according to claim 1 where in the at least two consensus sequences, the activator binding site upstream of the TATAAT sequence is selected from the group consisting of AGTT, TATTC, TG, TTGA, TTGG, TTAGCACTC and GAGTGCTAA.

24. (New) A set of promoters according to claim 23 where the sense strand of the double stranded DNA sequence comprises the motif GTACTGTT as a further consensus sequence.

25. (New) A set of promoters according to claim 1 where, when the selected organism or group of organisms is eukaryotic, the TATA-box is the TATAAA sequence.

26. (New) A set of promoters according to claim 25 where, when the selected organism or group of organisms is eukaryotic, the sense strand of the double stranded DNA sequence comprises the sequence CTCTTAACTGACTGCGA as further consensus sequence.

27. (New) A set of promoters according to claim 1 where, when the selected organism or group of organisms is eukaryotic, the UAS is UAS_{GCN4p}.

28. (New) A set of promoters according to claim 28 where, when the selected organism or group of organisms is eukaryotic, the sense strand of the double stranded DNA sequence comprises the sequence CTCTTAACTGACTGCGA as further consensus sequence.

REMARKS